

9904247\_4.Dn AAAAGTTCAAATCAAAGAAACATACAAAACACTACGTTTATATCAATTACAT

|||||

Scyol1110w AAAAGTTCAAATCAAAGAAACATACAAAACACTACGTTTATATCAATTAAATA  
1360 1370 1380 1390 14009904247\_4.Dna  
Emfun:ScchrXV44

ID SCCHRXV44 standard; DNA; FUN; 44019 BP.

AC Z48149;

SV Z48149.1

DT 03-FEB-1995 (Rel. 42, Created)

DT 24-MAR-1997 (Rel. 51, Last updated, Version 7)

DE S.cerevisiae chromosome XV DNA (44 kb fragment)

KW retrotransposon; sufl(+) frameshift suppressor; tRNA-Gly; tRNA-Thr; Tyl-H3.

OS Saccharomyces cerevisiae (baker's yeast)

OC Eukaryota; Fungi; Ascomycota; Saccharomycetes; Saccharomycetales;

OC Saccharomycetaceae; Saccharomyces.

RN [1]

RP 1-44019

RX MEDLINE; 96076631.

RA Vandenbol M., Durand P., Portetelle D., Hilger F.;

RT "Sequence analysis of a 44 kb DNA fragment of yeast chromosome XV including

RT the Tyl-H3 retrotransposon, the sufl(+) frameshift suppressor gene for

RT tRNA-Gly, the yeast transfer RNA-Thr-1a and a delta element.";

RL Yeast 11:1069-1075(1995).

RN [2]

RP 1-44019

RA Hilger F.;

RT ;

RL Submitted (31-JAN-1995) to the EMBL/GenBank/DBJ databases.

RL Hilger F., Faculte des Sciences Agronomiques de Gembloux, UER de

RL Microbiologie, Avenue Marechal Juin, 6, 5030 Gembloux, Belgium

RN [3]

RP 1-44019

RA John T.R., Ghosh M., Johnson J.D.;

RT "Identification and expression of the Saccharomyces cerevisiae cytoplasmic

RT tryptophanyl-tRNA synthetase gene";

RL Yeast 13:37-41(1997).

DR SPTREMBL; Q05377; Q05377.

DR SPTREMBL; Q05378; Q05378.

DR SPTREMBL; Q05379; Q05379.

DR SPTREMBL; Q12215; Q12215.

DR SPTREMBL; Q12239; Q12239.

DR SPTREMBL; Q12272; Q12272.

DR SPTREMBL; Q12285; Q12285.

DR SPTREMBL; Q12317; Q12317.

DR SPTREMBL; Q12348; Q12348.

DR SPTREMBL; Q12366; Q12366.

DR SPTREMBL; Q99393; Q99393.

DR SWISS-PROT; P13902; INO4\_YEAST.

DR SWISS-PROT; P22148; MSN1\_YEAST.

DR SWISS-PROT; P27680; COQ3\_YEAST.

DR SWISS-PROT; P30606; ITR2\_YEAST.

DR SWISS-PROT; P41912; SHR5\_YEAST.

DR SWISS-PROT; P53632; TRF4\_YEAST.

DR SWISS-PROT; Q12109; SYWC\_YEAST.

DR SWISS-PROT; Q12236; KOKO\_YEAST. . . .

SCORES Init1: 2485 Initn: 2485 Opt: 2485 z-score: 1959.1 E(): 0  
100.0% identity in 497 bp overlap

10

20

30

9904247\_4.Dn

GGAGGTCTGCTTCACGAGCGCGGTGTGCGC

Scchr xv44 GAGCAGTACGTGGCGCAGCTAAACTCGCCGGGAGGTCTGCTTCACGAGCGCGGTGTGCGC  
12850 12860 12870 12880 12890 12900

9904247\_4.Dn CTAGTATTGCCCCGACGGTCCGGGTGCCTATCCCTAGATTTTCGTGCTGCCCCGACCCAAA  
40 50 60 70 80 90  
Scchr xv44 CTAGTATTGCCCCGACGGTCCGGGTGCCTATCCCTAGATTTTCGTGCTGCCCCGACCCAAA  
12910 12920 12930 12940 12950 12960

9904247\_4.Dn TAGTTAAACGTGTGGTTTATGGGTGCACCAGGGCTTTATCGTGTTTTATATCGATGGCGA  
100 110 120 130 140 150  
Scchr xv44 TAGTTAAACGTGTGGTTTATGGGTGCACCAGGGCTTTATCGTGTTTTATATCGATGGCGA  
12970 12980 12990 13000 13010 13020

9904247\_4.Dn TTTGTGCCTCCAGTGTATTTTTGTATATCCAATTAAGGTTTCTTACCTAATTTTATTTTT  
160 170 180 190 200 210  
Scchr xv44 TTTGTGCCTCCAGTGTATTTTTGTATATCCAATTAAGGTTTCTTACCTAATTTTATTTTT  
13030 13040 13050 13060 13070 13080

9904247\_4.Dn ATCATCTTTAGTTAATGCTGGTTTGCTCTGTTTCTGCTGCTTTCTGTGCGGTTCTCCTCT  
220 230 240 250 260 270  
Scchr xv44 ATCATCTTTAGTTAATGCTGGTTTGCTCTGTTTCTGCTGCTTTCTGTGCGGTTCTCCTCT  
13090 13100 13110 13120 13130 13140

9904247\_4.Dn TCTCTTGTCTTCTTCGTGTTGTCCCCCATCGCCGATGGGCTTATATGGCGTATATATATAG  
280 290 300 310 320 330  
Scchr xv44 TCTCTTGTCTTCTTCGTGTTGTCCCCCATCGCCGATGGGCTTATATGGCGTATATATATAG  
13150 13160 13170 13180 13190 13200

9904247\_4.Dn AGCGAGTTTTTACGTCGAAGATCATCTCAGTTTGCTTGATAGCCTTTCTACTTTATTACT  
340 350 360 370 380 390  
Scchr xv44 AGCGAGTTTTTACGTCGAAGATCATCTCAGTTTGCTTGATAGCCTTTCTACTTTATTACT  
13210 13220 13230 13240 13250 13260

9904247\_4.Dn TTCGTTTTTAACCTCATTATACTTTAGTTTTCTTTGATCGGTTTTTTTCTCTGTATACTT  
400 410 420 430 440 450  
Scchr xv44 TTCGTTTTTAACCTCATTATACTTTAGTTTTCTTTGATCGGTTTTTTTCTCTGTATACTT  
13270 13280 13290 13300 13310 13320

9904247\_4.Dn AAAAGTTCAAATCAAAGAAACATACAAAACACTACGTTTATATCAATTACAT  
460 470 480 490 500  
Scchr xv44 AAAAGTTCAAATCAAAGAAACATACAAAACACTACGTTTATATCAATTAAATAATGTCTGAAA  
13330 13340 13350 13360 13370 13380

Scchr xv44 TTCAAAACAAAGCTGAAACTGCCGCCCAAGATGTCCAACAAAAGTTGGAAGAAACCAAAG  
13390 13400 13410 13420 13430 13440

9904247\_4.Dna /rev  
Emgss9:Aq875364

ID AQ875364 standard; DNA; GSS; 470 BP.  
AC AQ875364;  
SV AQ875364.1  
DT 09-NOV-1999 (Rel. 61, Created)  
DT 09-NOV-1999 (Rel. 61, Last updated, Version 1)